AMENDMENTS TO THE SPECIFICATION

Please replace the following paragraphs after "BRIEF DESCRIPTION OF THE DRAWINGS" as follows:

Please replace the paragraph beginning on page 6, line 9 with the following amended paragraph:

Figure 1A – 1F depicts physical maps of the VRN1 regions of various plants. **Figure 1A** depicts a genetic map of the *VRN1* region on chromosome $5A^m$ of *T. monococcum*. Genetic distances are in cM (6,190 gametes). **Figure 1B-D** depict physical maps of the collinear *VRN1* regions in rice, sorghum, and wheat. Regions indicated in red have been sequenced. Double dot lines indicate gaps in the current physical maps. **Figure 1B** shows the sequence of the collinear region in rice chromosome 3. **Figure 1C** shows *S. bicolor* BACs 170F8 (AF503433) and 17E12 (AY188330). **Figure 1D** shows a *T. monococcum* physical map. BAC clones order from left to right is: 49I16, **115G1**, 136F13, 133P9, **116F2**, 89E14, 160C18, 491M20, 328O3, **609E6**, 393O11, **719C13**, 454P4, 54K21, 579P2, 601A24, **231A16**, 638J12, 52F19, 242A12, 668L22, 539M19, and 309P20 (bold letters indicate sequenced BACs). Black dots indicate validation of BAC connections by hybridization. **Figure 1E** shows the gene structure of two MADS-box genes completely linked to the *VRN1* gene (AY188331, AY188333). Bars represent exons. **Figure 1F** shows the sequence comparison of the *AP1* promoter regions from genotypes carrying the *Vrn1* and *vrn1* alleles, and from two *T. monococcum* accessions with additional deletions (SEQ ID NO: 1-4). Deletions in the promoters in SEQ ID 2 and 3 have been found to be completely linked to the *Vrn1* allele for spring growth habit. Linkage between SEQ ID 4 and the *Vrn1* allele for spring growth habit has not been determined yet. Numbers indicate distances from the start codon. A putative MADS-box protein-binding site (CArG-box) is highlighted.

Please replace the paragraph beginning on page 7, line 28 with the following amended paragraph:

Figure 7A-7B depicts allelic variation in the diploid wheat AP1 DNA sequences. The bolded and underlined nucleotide indicates the only polymorphism in the coding region. ~~Figure 7A~~ Figure 7A depicts the sequence of G2528 (*vrn1*) = DV92 (*vrn1*) (SEQ ID NO:5). ~~Figure 7B~~ Figure 7B depicts the sequence of G1777 (*vrn1*) = G3116 (*vrn1*) (SEQ ID NO:6).

Please replace the paragraph beginning on page 8, line 3 with the following amended paragraph:

Figure 8A-8B depicts allelic variation in the wheat AP1 protein sequence. The bolded and underlined amino acid indicates a difference in the sequence. ~~Figure 8A~~ Figure 8A depicts the sequence of G2528 (*vrn1*) = DV92 (*vrn1*) (SEQ ID NO:7). ~~Figure 8B~~ Figure 8B depicts the sequence of G1777 (*vrn1*) = G3116 (*vrn1*) (SEQ ID NO:8).

Please replace the paragraph beginning on page 81, line 18 with the following amended paragraph:

RNA interference

The RNAi construct was made in the binary vector pMCG161 (available on the Internet at ~~www.chromdb.org/mcg161.html~~ the website for the Plant Chromatin Database, ChromDB). This vector contains a cassette designed for making inverted repeat transcripts of a gene, flanking a loop, which should efficiently produce a double stranded RNA. Expression of the transgene is driven by the 35S promoter followed by the *Adh1* intron.